

Commissioner is hereby authorized to deduct the necessary fees from Fulbright & Jaworski L.L.P. Account No.: 50-1212/10008123/TMB.

I. AMENDMENT

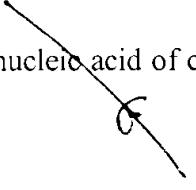
In the Specification:

Please amend the specification at page 2 by replacing the first paragraph with the following paragraph:

This is a continuation-in-part of application Serial No. 60/000,831, filed July 3, 1995.

In the Claims:

Please amend the claims as follows:

91. The isolated nucleic acid of claim 90, wherein said nucleic acid is up to 10,000 basepairs in length.
- 

II. REMARKS

The present amendment corrects the antecedent basis for claim 91 and corrects a typographical error introduced by the preliminary amendment of August 19, 1999. Entry of this Amendment is requested in order to place the claims in a better position for appeal under 37 C.F.R. §1.116. No new matter is introduced by these amendments.

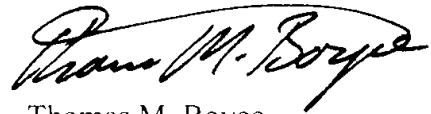
A marked copy of the claims for amendment is provided as Appendix A. For the convenience of the Examiner, a copy of the pending claims as amended is provided as Appendix B. A marked copy of the amended paragraph of the specification is provided as Appendix C.

III. CONCLUSION

Applicants have submitted amendments and remarks which are believed to place the present claims in better condition for appeal.

Please date stamp and return the enclosed postcard evidencing receipt of these materials.

Respectfully submitted,



Thomas M. Boyce
Reg. No. 43,508
Attorney for Applicants

FULBRIGHT & JAWORSKI, LLP
600 Congress Avenue, Suite 2400
Austin, Texas 78701
(512) 536-3043

Date: June 7, 2002

APPENDIX A: CLAIMS MARKED FOR AMENDMENT

91. (Amended) The isolated nucleic acid of claim [88]90, wherein said nucleic acid is up to 10,000 basepairs in length.

APPENDIX B: PENDING CLAIMS AFTER AMENDMENT

39. An isolated nucleotide comprising a sequence region that encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2.
40. The isolated nucleotide of claim 39, wherein said sequence region comprises at least 21 contiguous nucleotides from nucleotide 122 to nucleotide 970 of SEQ ID NO:1.
41. The isolated nucleotide of claim 40, wherein said sequence region comprises at least 30 contiguous nucleotides from nucleotide 122 to nucleotide 970 of SEQ ID NO:1.
42. The isolated nucleotide of claim 41, wherein said sequence region comprises at least 40 contiguous nucleotides from nucleotide 122 to nucleotide 970 of SEQ ID NO:1.
43. The isolated nucleotide of claim 42, wherein said sequence region comprises the sequence from nucleotide 122 to nucleotide 970 of SEQ ID NO:1.
44. The isolated nucleotide of claim 42, comprising the sequence of SEQ ID NO:1.
45. The isolated nucleotide of claim 39, wherein said polypeptide promotes melanoma senescence.
46. The isolated nucleotide of claim 39, wherein said polypeptide suppresses glioma cell tumor generation.
47. The isolated nucleotide of claim 39, wherein said nucleotide is from about 849 to about 5,000 basepairs in length.
48. The isolated nucleotide of claim 47, wherein said nucleotide is from about 849 to about 3,000 basepairs in length.

49. The isolated nucleotide of claim 48, wherein said nucleotide is from about 849 to about 1,000 basepairs in length.
50. The isolated nucleotide of claim 39, wherein said coding region is operably positioned under the control of a promoter.
51. The isolated nucleotide of claim 39, wherein said coding region is operatively linked to a second coding region that encodes a selected peptide or polypeptide, said nucleotide encoding a methylthioadenosine phosphorylase fusion peptide or polypeptide.
52. The isolated nucleotide of claim 39, comprised within a vector.
53. The isolated nucleotide of claim 39, comprised within a host cell.
54. A nucleic acid of from about 850 to about 10,000 nucleotides in length comprising a nucleotide sequence encoding a methylthioadenosine phosphorylase polypeptide, said polypeptide comprising a sequence region of at least about 10 contiguous residues from SEQ ID NO:2.
55. The nucleic acid of claim 54, wherein said polypeptide comprises a sequence region of at least about 20 contiguous residues from SEQ ID NO:2.
56. The nucleic acid of claim 55, wherein said polypeptide comprises a sequence region of at least about 30 contiguous residues from SEQ ID NO:2.
57. The nucleic acid of claim 54, wherein said nucleotide sequence is operably linked to a heterologous promoter.
58. The nucleic acid of claim 57, wherein said promoter is selected from the group consisting of a RSV, CMV, LTR, Sv40, *lac*, *trp*, *tac*, lacUV5, and a T7 promoter.

59. The nucleic acid of claim 57, comprised within a vector.
60. The nucleic acid of claim 57, comprised within a host cell.
61. An isolated nucleic acid segment of between about 21 and about 500 nucleotides in length that comprises a contiguous sequence from SEQ ID NO:1, or that specifically hybridizes to said contiguous sequence from SEQ ID NO:1 under stringent hybridization conditions.
62. The nucleic acid segment of claim 61, wherein said segment is between about 21 and about 300 nucleotides in length.
63. The nucleic acid segment of claim 62, wherein said segment is between about 21 and about 200 nucleotides in length.
64. The nucleic acid segment of claim 63, wherein said segment is between about 21 and about 100 nucleotides in length.
65. The nucleic acid segment of claim 61, comprised within a vector.
66. The nucleic acid segment of claim 61, comprised within a host cell.
67. A vector comprising at least a first nucleotide sequence that encodes a mammalian methylthioadenosine phosphorylase polypeptide comprising the amino acid sequence of SEQ ID NO:2.
68. The vector of claim 67, wherein said nucleotide sequence comprises the nucleic acid sequence of SEQ ID NO:1.
69. The vector of claim 67, comprised within a host cell.

70. A host cell comprising at least a first nucleotide sequence that encodes a mammalian methylthioadenosine phosphorylase polypeptide comprising the amino acid sequence of SEQ ID NO:2.
71. The host cell of claim 70, wherein said nucleotide sequence comprises the nucleic acid sequence of from about nucleotide 122 to nucleotide 970 of SEQ ID NO:1.
72. The host cell of claim 70, wherein said cell is a prokaryotic host cell.
73. The host cell of claim 70, wherein said cell is a eukaryotic host cell.
74. An isolated nucleotide comprising a nucleic acid sequence that encodes a methylthioadenosine phosphorylase polypeptide, wherein said isolated nucleotide hybridizes to an at least 21 nucleotide contiguous nucleic acid sequence from SEQ ID NO:1 under stringent hybridization conditions.
75. The isolated nucleotide of claim 74, wherein said polypeptide comprises a contiguous amino acid sequence from SEQ ID NO:2.
76. The isolated nucleotide of claim 74, wherein said isolated nucleotide encodes a human methylthioadenosine phosphorylase polypeptide.
77. A method of making a methylthioadenosine phosphorylase polypeptide, comprising the steps of:
- (a) obtaining a vector in which a gene encoding a polypeptide comprising a sequence region of at least about 10 contiguous amino acid residues from SEQ ID NO:2 is positioned under the control of a promoter;
- (b) introducing said vector into a host cell;

- (c) culturing said host cell under conditions effective to express said polypeptide; and
- (d) collecting said expressed polypeptide.

78. A method for detecting a nucleic acid segment comprising a sequence region encoding a methylthioadenosine phosphorylase polypeptide, comprising the steps of:

- (a) obtaining sample nucleic acids suspected of containing a sequence region encoding a methylthioadenosine phosphorylase polypeptide;
- (b) contacting said sample nucleic acids with a nucleic acid segment comprising at least 21 contiguous nucleotides of SEQ ID NO:1 under conditions effective to allow hybridization of substantially complementary nucleic acids; and
- (c) detecting the hybridized complementary nucleic acids thus formed.

79. The method of claim 78, wherein the sample nucleic acids contacted are located within a cell.

80. The method of claim 78, wherein the sample nucleic acids are separated from a cell prior to contact.

81. The method of claim 78, wherein the sample nucleic acids are DNA.

82. The method of claim 78, wherein said isolated nucleic acid segment comprises a detectable label and the hybridized complementary nucleic acids are detected by detecting said label.

83. The method of claim 82, wherein the nucleic acid segment comprises a radio-, enzymatic or fluorescent label.

84. A detection kit comprising, in suitable container means, a first nucleic acid segment comprising at least 21 contiguous nucleotides of SEQ ID NO:1 and a detection reagent.
85. The detection kit of claim 84, further comprising at least a first restriction endonuclease.
86. The detection kit of claim 84, further comprising a second nucleic acid segment comprising at least 21 contiguous nucleotides of SEQ ID NO:1.
87. The detection kit of claim 84, wherein said detection reagent is a detectable label that is linked to said nucleic acid segment.
88. An isolated nucleic acid that:
- (a) comprises a sequence region that consists of at least 21 contiguous nucleotides that have the same sequence as, or are complementary to, 21 contiguous nucleotides of SEQ ID NO:1; or
- (b) is a nucleic acid of from 21 to 10,000 nucleotides in length that hybridizes to a contiguous nucleotide sequence from SEQ ID NO:1; or the complement thereof, under stringent hybridization conditions.
89. The isolated nucleic acid of claim 88, that comprises a sequence region that consists of at least 14 contiguous nucleotides that have the same sequence as, or are complementary to, 21 contiguous nucleotides of SEQ ID NO:1.
90. The isolated nucleic acid of claim 88, that is from 21 to 10,000 nucleotides in length that hybridizes to a contiguous nucleotide sequence from SEQ ID NO:1, or the complement thereof, under stringent hybridization conditions.
91. The isolated nucleic acid of claim 90, wherein said nucleic acid is up to 10,000 basepairs in length.

92. The isolated nucleic acid of claim 91, wherein said nucleic acid is up to 5,000 basepairs in length.
93. The isolated nucleic acid of claim 92, wherein said nucleic acid is up to 3,000 basepairs in length.
94. The isolated nucleic acid of claim 93, wherein said nucleic acid is up to 1,000 basepairs in length.

APPENDIX C: SPECIFICATION PARAGRAPH MARKED FOR AMENDMENT

This is a continuation-in-part of application Serial No. 60/000,831, filed July [2]3, 1995.